0.71

1283 1283 1283

aj275971.res

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1. aj275971
                                                                                Sequence Name
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                                                                                                            Results file aj275971.res made by bobryen on Tue 17 Jun 103 9:07:04-PDT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Init. Opt.
Length Score Score
                                                                                                                                                                                                                     Results of the initial comparison of aj275971 (1-1283) with: File : genbank.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Standard Deviation 74.95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570 713 855 998 1140
-9 -8 -7 -6 -5 -4 -3 -2 -1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total Elapsed 00:00:00:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 100% identical sequence to the query sequence was found:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K-tuple
Joining penalty
Window size
                                                                                                                                                          aj275971 (1-1283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The scores below are sorted by initial score.
Significance is calculated based on initial score.
                                                              FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEARCH STATISTICS
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1178
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2
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00:00:00
                                                                                                                                                        Query sequence being compared:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.00
0.33
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Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mean
1230
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> 0 < 0 | O IntelliGenetics > 0 < 0 | O Intelligenetics > 0 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCORE 0
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Scores:

Times:

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Sig. Frame
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650 660 670 680 690 700 710 720 CCAACTCCCACAAAGGACAGGGAGGGAACCTCTCACCGAGGTGTGATCAAGTGGCTGAGCGTCAACCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -0.71
                                                                                                                                                                                                                                                                                                                                                                                                       0.71
                                                                                                                            Init. Opt.
Length Score Score
                                                                                                                                                                                                               1355 1177 1203
                                                                                                                                                                                                                                                                                                                                                                                                       Optimized Score = 1283 Significance
Matches = 1283 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                               from: 1 to: 1283
TOIG of: aj275971 check: 448
                                                                                                                                                                                              TOIG of: aj275972 check: 350
                                                                                                                                                                                                                                                                                                                                            of: aj275971 check: 4487
                                                           best scores is:
                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                          1283
100%
                                                                                                                                                                                                                                                                                                              1. aj275971 (1-1283)
aj275971 TOIG
                                                                                                                                                                                                                                                                                                                                                                                                       Initial Score = Residue Identity = Gaps =
                                                           The list of other
                                                                                                                                                                                              2. aj275972
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	810 850 860 ATGTCTTGCAAGCTGTTCATCCTTTGTCTGCTCATCGTGGGTTCTTAGGTTGTAAGCACTTCTCCA ATGTCTTGCAAGCTGTTCATCCTTTGTCTGCTCATCGTTGGTTG	870 880 930 AGGCTAACGGGCTGCTGAAACTATCTGGGACGGACGGACCTATAAACTGGAGGAGCACTCTTAATGCTGC	940 950 CTTATACTGTTATAGATGAACATCACATATATTTCTACAGCTTTTCCAAGTTCAAACCAATC CTTATACTGTTAACTGTTTTAAGATGAACATCACACTATATTTTCTACAGCTTTTCCAAGTTCAAACCAATC CTTATACTGTTAACTGTTTTAAGATGAACATCACACTATATTTTCTACAGCTTTTCCAAGTTCAAACCAATC 940 950 950 950 960	1010 1020 1030 1040 1050 1060 1070 1080 TATAAGCTITCATTIGGAATGATGCTGCTTTTTGGTCGGTTTTTAGATACTTTAAAAACACTTTAACAC	1090 1100 1150 1150 1150 1150 1150 1150	1160 1170 1180 1220 1220 1220 1220 1220 1220 122	1230 1240 1250 1260 1270 1280 X - ACCTATITICATGACTGCTAAGTITITATGCAGAAATAAATTATATATTTA	2. aj275971 (1-1283) aj275972 TOIG of: aj275972 check: 3502 from: 1 to: 1355	Initial Score = 1177 Optimized Score = 1203 Significance = -0.71 Residue Identity = 94% Matches = 1216 Mismatches = 61 Gaps = 11 Conservative Substitutions = 0	20 X 10 20
		800 810 820 830 840 RGTCTTGCAAGCTGTTCATCCATCCTTTGTTTGTTTGTTTG	810 820 850 850 860		### ##################################	### ##################################			1000	

100

90

aj275971.res

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/trānslation="MLFKLGLCQRCISSNRVLPGLLIPQTLCFSKLMKITPKKLRSSN
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MSFVADERSRHTVYPPADQVYSWTEMCDIQDVKVVILGQDPYHGPNQAHGLCFSVQKP
                                                 GMO275971 1283 bp mRNA linear VRT 07-JUN-2002 Gadus morhua mRNA for uracil-DNA glycosylase precursor (ungl gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPPPPSLVNIYKELCTDIDGFKHPGHGDLSGWAKQGVLLLNAVLTVRAHQANSHKDRG
WETFTDAVIKWLSVNREGVVFLLWGSYAHKKGATIDRKRHHVLQAVHPSPLSAHRGFL
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                          Lanes, O., Leiros, I., Smalas, A.O. and Willassen, N.P.
Identification, cloning, and expression of uracil-DNA glycosylase
from Atlantic cod (Gadus morhua): characterization and homology
modeling of the cold-active catalytic domain
Extremophiles 6 (1), 73-86 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-MAR-2000) Lanes O., Department of Biotechnology, University of Tromsoe, Institute of Medical Biology, Medical Faculty, N-9037, NORWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.275971-pep 1
DIRLOICCSS. GYAKDAYHQIGSYQVY. PPKLYVFLN..R. RRRN. GPQMMNKRRHRHSFQWSSWKEWPK
IRKQRICTRLEQXQCAYCHSTRLOKGRGCCTFRG.
K..F.ARTLITVPTKHMDSVSVCKSQFPLPPVS. TYTKNCVFTLMASSILDMEI. ADGQNKGCCCLTRC.
PCGPIRPTPTREAGRPSPTL. SSG. AGTGKEWFSCCGAHTPIRRERPSTGNYTMSCKLFIHLLCLIVG
SLVVSTSPRLTGC. NYLGRSL. TGEHSNSLCCLILLTVLR. TSHYIFYSFKFPIYKLSFVFWNDAAFG
RF. ILKTLYHSAMLTHVQSI. LSQLEQKCYFIIDYILYIKDCFPPRLFRRY. DIKLLLTYFP. CQLLKFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Check: 4487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="uracil-DNA glycosylase precursor"
                                                                                                                                                 precursor; UNG1 gene; uracil-DNA glycosylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  June 17, 2003 08:47 Type: N
     to: 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB85707.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCKHFSKANGLLKLSGTEPINWRAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gadus morhua"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:8049"
/tissue_type="liver"
/dev_stage="adult"
/country="Norway"
  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EC number="3.2.2.3" codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                         AJ275971.1 GI:7413911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="ung1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="ung1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 1283)
  check: 4487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                           Atlantic cod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 1283
                                                                                                     AJ275971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11878565
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21867342
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TOIG of: aj275971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                 LOCUS
DEFINITION
                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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AJ275971-pep_2
TSACKYVVOKTWIPKOHIIKSGLTRFTNSPNFMFF.INEDNAEETEVLKCGTKDVIATAFSGAAGKNGQK
ESSA QD. SKSNACRFRRDLEKRAGCRV.KAILQTIDVLCS. . EEPSHRLPTG.SSVQLDRDV.HSRCE
SSDSRPGPLPRSQPSTWTLFQCAKASSPSPGSREHIORIVYRH.WLQASWTWRSKRMGKTRGAAA.RGAD
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AEINYIF1

AJ275971-pep 3 - Frame 3 HPLANMLFKGGLÖGRCISSNRVLPGLLIPQTLCFSKLMKITPKKLRSSNVEQKTSSPQLSVEQLERMAKN

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VRT 07-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSFVADERSRHTVY PPADQVYSWTEMCDIODVKVVILGQDPYHGPNOAHGLCFSVQŘP
VPPPPSLVNI YKELCTDIDGFKHPGHGDLSGWAKQGVLLLNAVLTVRAHQANSHKDRG
WETFTDAVI KWLSVNREGVVFLLWGSYAHKKGATIDRKRHHVLQAVHPSPLSAHRGFL
                                                                                                                                                                                                                                                GMOZ/5972 1355 bp mRNA linear VRT 07-JUN-200;
Gadus morhua mRNA for uracil-DNA glycosylase precursor (ung2 gene).
AJ275972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii; Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Paracanthopterygii, Gadiformes, Gadidae, Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification, cloning, and expression of uracil-DNA glycosylase from Atlantic cod (Gadus morhua): characterization and homology modeling of the cold-active catalytic domain Extremophiles 6 (1), 73-86 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lanes O., Department of Biotechnology, Institute of Medical Biology, Medical
                        VVIIGQDPYHGPNQAHGLCFSVQKPVPPPPSLVNIYKELCTDIDGFKHPGHGDLSGWAKQGVLLLNAVLT
VRAHQANSHKDRGWETFTDAVIKWLSVNREGVVFLLWGSYAHKKGATIDRKRHHVLQAVHPSPLSAHRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPQMMNKRRHRHSFQWSSWKEWPKIRKQRLTRLEQKQRLQVSERLGEESWLQSLKSHTSNN.CPL.LMRG
AVTPSTHRLIKCTVGQRCVTFKM.K.F.ARTLTTVPTKHMDSVSVCKSQFPLPPVS.TYTKNCVPTLMA
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FYSFGKRFPYKLSFVFWNDAAFGRF.LLKTLYHSAMLTHVQSI.LSGLEQKCYFIIDYILYIRDFFPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ275972-pep_2
MV.EDSTLTLVSEGENGVIVHIVLALRLKNDWSTAYQLFLLTSFKKESFKGIR.NRKACRRSSDNAEETE
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PSHRLPTG.SSVQLDRDV.HSRCESSDSRPGPLPRSQPSTWTLFQCAKASSPSPGSREHIQRIVYRH.WL
                                                                                    LGCKHFSKANGLLKLSGTEPINWRAL. LFMLPYTVNCFKMNITLYFLQLFQVQTNL. AFICLLE. CCFWS
VLDT. NTLPLCHVDSCSVNITFTT. TKMLFYN. LYSVH. RLFFSQAVS. VLGY. TVINLFSMMSTA. VFM
KKAALDKI RAKATPAGFGETWRRELAAEFEKPY FKOLMS FVADERSRHTVY PPADQVY SWTEMCDI QDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AJ275972-pep_1
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DGLGG.YFDTG.REGERESYCAYRFSPTFKK.LVNSISTLSSHQFOKREFORN.OKPKSMPKFR.CRESYLOSLKSHTSNN.CPL.LMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 1355 June 17, 2003 08:48 Type: N Check: 3502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smalas, A.O. and Willassen, N.P.
                                                                                                                                                                                                                                                                                                                                                          AJ275972.1 GI:7413913
precursor; ung2 gene; uracil-DNA glycosylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="uracil-DNA glycosylase"
                                                                                                                                                                                                           TOIG of: aj275972 check: 3502 from: 1 to: 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-MAR-2000) Lanes O., University of Tromsoe, Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Gadus morhua"
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/country="Norway"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       number="3.2.2.3"
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ACCESSION
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TITLE
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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QASWTWRSKRMGKTRGAAA.RGADRAGPSGQLPQGQRLGDLHRRCDQVAERQFGRSGFPVVGLIRP.BGS
DHRQETGSGSLSRVCSSISPVCSSWVPWL.ALLQG.RAAETIWDGAYKLESTLTLYAALYC.LF.DEHHTIF
STAFPSSNQSISFULSFGMMLLLVGFRYLKHFTTLPC.LMFSQYNFHNLNKNVIL.LIIFCTLKIVFFPG
CPIGTRILNCY.PIFHDVNCLSFYAEINYIF1

AJ275972-ppp 3 for frame 3
WFRIVL. HWLAKGKTELLCISF. PYV. KMIGQQHINSFFSPVSKKRVSKELGKTEKHAEEVQITPKKLR
SSNVEQKTSSPQLSVEDLERMAKUKKALDKITAKATPAGFGETWRRELAAEFEKPYFKQLMSFVADERS
RHTVYPPADQVYSWTEMCDIQDVKVVILGQDPYHGPNQAHGLCFSVQKPVPPPPSLVNIYKELCTDIDGF
KHPCHGADSGWARGOVLLLANATTVRAHQANSHYDRGWETFIDAVIKWLSVNREGVVFLLMGSYAHKKGA
KHPCHGADSGWARGOVLLLANATTVRAHQANSHYDRGWETFIDAVIKWLSVNREGVVFLLMGSYAHKKGA
LOLDRKRHHVLQAVHPSPLSAHGFLGCKHFSKANGLLKLSGTEPINWRAL. LFMLPYTVNCFKWNITLYF
LOLDRKRHHVLAAFLCLE. CCFWBVLDT. NTPLCHVDSCSVNITFTT. TKMLFYN. LYSVH. RIFFSQA
VS. VLGY. TVINLFSMMSTA. VFMQK. I IY1

trans.pep

Sig. Frame

392

Init. Opt. Length Score Score

0

1.39

415

415

415

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**** 1 standard deviation above mean ****
                                      The list of other best scores is:
                                                                                                                                                                                                                                                                                                                       100
                                                                            Description
                                                                                                                                                                                          415
100%
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375
91%
0
                                                                                                                                                    1. AJ275971-pep_3 (1-426)
AJ275971-pep_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2. AJ275971-pep_3 (1-426)
AJ275972-pep_3
                                                                                                              2. AJ275972-pep_3
               1. AJ275971-pep_3
                                                                                                                                                                                         Initial Score = Residue Identity = Gaps ': =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Score = Residue Identity = Gaps
                                                                            Sequence Name
                                                                                                                                                                                                                                                                                                                       80
                                                                                      Results file aj275971-pep_3.res made by bobryen on Tue 17 Jun 103 9:10:30-PDT.
                                                                                                                                                                          Results of the initial comparison of AJ275971-pep_3 (1-426) with: File : trans.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Standard Deviation 196.66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total Elapsed 00:00:00:00
                                                                                                                          Query sequence being compared:AJ275971-pep_3 (1-426)
Number of sequences searched:
6
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277
                                                FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEARCH STATISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Median
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231
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6
6
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00:00:00
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0.05
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141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences searched:
scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138
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-2
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Gap penalty
Gap size penalty
Cutoff score
Randomization group
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Threshold level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -46
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290 340 350 360 360 350 AMGLIKLSGTEDINWRALLFWLPYTVNCFKWNTLYFDQLFQVQTNLAFICLLECCFWSYLDTNTLPLCHVD AMGLIKLSGTEDINWRALLFWLPYTVNCFKWNTTLYFLQLFQVQTNLAFICLLECCFWSYLDTNTLPLCHVD AMGLIKLSGTEDINWRALLFWLDYTVNCFKWNTLYFLQLFQVQTNLAFICLECCFWSYLDTNTLPLCHVD 300 310 320 340 350
                                                    QKTSSPQLSVEQLERMAKNKKAALDKI RAKATPAGFGETWRELAAEFEKPYFKQLMSFVADERSRHTVYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKTSSPQLSVEQLERMAKNKKAALDKIRAKATPAGFGETWRRELAAEFEKPYFKQLMSFVADERSRHTVYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSIGNATION TO TO TO TO TO THE HELANMLEKLGLCORCISSNRVLPGLLIPOTICFSKLMKITFKKLRSSNRVF
1.39
Optimized Score = 415 Significance
Matches = 415 Mismatches
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimized Score = 392 Significance
Matches = 379 Mismatches
Conservative Substitutions
                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCSVNITETITYMLEYNLYSVHRLFFSQAVSVLGYTVINLFSHMSTAVFMQKIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90
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Init. Opt. Length Score Score Sig. Frame

A 100% identical sequence to the query sequence was found:

Description

Sequence Name

The scores below are sorted by initial score. λ Significance is calculated based on initial score.

Scores:

Times:

140	190 DGFKHPGHGDLS DGFKHPGHGDLS 210	260 KKGATIDRKRHHVLQ KKGATIDRKRHHVLQ 280	330 OLFQVQTNLAFIC OLFQVQTNLAFIC OLFQVQTNLAFIC 350	360 400 410
130		250 .LWGSYAHKKG; .LWGSYAHKKG; .LWGSYAHKKG; 270	320 VNCFKANITLYFLQI VNCFKANITLYFLQI 340	400 VSVLGYTVINL)
120	170 QKPVPPPPSLVNIYKEI 	240 LSVNREGVVFLLWGSYAHI LSVNREGVVFLLWGSYAHI 260	310 LEMLPYTUNCF L LEMLPYTUNCF 330	380 LYSVHRLFFSQAVSV LYSVHRLFFSQAVSV
110	160 QAHGLCFSV QAHGLCFSV 180	₹ =₹	300 LSGTEPINWRAL) LSGTEPINWRAL) 320	370 380 ITETTTKALFYNLYSVH ITETTKALFYNLYSVH 390 400
100	150 /ILGQDPYHGPN /ILGQDPYHGPN	220 QANSHKDR QANSHKDR 240	290 CKHFSKANGLLKLS CKHFSKANGLLKLS 310	360 37 CHVDSCSVNITFT CHVDSCSVNITFT 380 390
06	130 ADQVYSWTEMCDIQDVKVV 	210 LNAVLTVRAH LNAVLTVRAH 230	280 SAHRGFLGCKHF SAHRGFLGCKHF 300	350 360 VLDTNTLPLCHVI VLDTNTLPLCHVI 70 380
80	130 ADQVYSWTEM ADQVYSWTEM 150	200 GWAKQGVLL GWAKQGVLL 220	270 AVHPSPLSA AVHPSPLSA 290	340 350 LLECCFWSVLDTN/ LLECCFWSVLDTN/ 370
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